SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> FILAMENTOUS FUNGAL MUTANTS WITH IMPROVED HOMOLOGOUS RECOMBINATION
EFFICIENCY

<130> 24181WO

<160> 17

<170> PatentIn version 3.1

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<212> DNA
<213> Aspergillus niger

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ctccccgaaa aaccagaaga caaaaccatt ccgaaatacc gccaaatcga caagcgcgcc   1620

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Phe Ala Ile Asp Val Ser Asp Ser Met Leu Thr Pro Arg Pro Ser Ala
            35   40   45

Asp Pro Lys Lys His Thr Gln Glu Ser Pro Thr Thr Ala Ala Leu Lys
    50   55   60

Cys Ala Tyr His Phe Met Gln Gln Arg Ile Ile Ser Asn Pro Gln Asp
65   70   75   80

Met Met Gly Val Leu Leu Phe Gly Thr Gln Ala Ser Lys Phe Phe Glu
            85   90   95

Glu Asp Glu Asp Ser Arg Gly Asp Leu Ser Tyr Pro Asn Cys Tyr Leu
            100   105   110

Phe Thr Asp Leu Asp Val Pro Ser Ala His Glu Val Lys Gly Leu Arg
            115   120   125

Ala Leu Val Asp Asp Glu Gly Asp Ser Arg Glu Val Leu Ser Pro Ala
    130   135   140

Lys Glu Gln Val Ser Met Ala Asn Val Leu Phe Cys Ala Asn Gln Ile
145   150   155   160

Phe Thr Ser Arg Ala Pro Asn Phe Leu Ser Arg Arg Leu Phe Ile Ile
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            180   185   190

Ala Thr Val Arg Ala Lys Asp Leu Tyr Asp Leu Gly Val Thr Ile Glu
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Tyr Asp Ser Leu Pro Ser Asp Pro Glu Ala Pro Ala Tyr Leu Gln Ser
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Asp Ser Lys Ala Ala Thr Ala Thr Gly Asp Gly Ile Ser Leu Leu Asn
            245             250             255

Thr Leu Leu Ser Ser Ile Asn Ser Arg Thr Val Pro Arg Arg Thr His
            260             265             270

Phe Ser Asn Met Pro Leu Glu Leu Gly Pro Asp Phe Arg Ile Ser Val
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Ser Gly Tyr Ile Leu Leu Arg Arg Gln Ala Pro Ala Arg Asn Ser Phe
    290             295             300

Ile Trp Leu Asn Gly Glu Lys Pro Val Val Ala Lys Gly Val Thr Ser
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His Ser Ala Asp Asp Thr Gly Arg Thr Val Glu Lys Trp Glu Ile Arg
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Lys Ala Tyr Lys Phe Gly Gly Asp Gln Val Thr Phe Ser Pro Asp Glu
        340             345             350

Gln Lys Ala Leu Arg Asp Phe Gly Glu Pro Val Ile Arg Val Ile Gly
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Phe Lys Pro Ile Thr Ala Leu Pro Phe Trp Ala Asn Val Lys His Pro
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Tyr Phe Ile Tyr Pro Ser Glu Glu Asp Tyr Val Gly Ser Ser Arg Val
385             390             395             400

Phe Ser Ala Leu His Gln Thr Leu Leu Arg Ser Lys Lys Met Ala Leu
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Val Trp Phe Ile Ala Arg Lys Gly Ala Gly Pro Val Leu Ala Ala Met
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Ile Ala Gly Glu Glu Lys Leu Asp Glu Asn Gly Val Gln Lys Tyr Pro
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Asn Pro Glu Thr Thr Leu Asn Val Ala Pro Glu Ser Leu Ile Asp Gln
465             470             475             480

Met Arg Val Ile Val Gln Gln Leu Gln Leu Pro Lys Gly Val Tyr Glu
            485             490             495

Pro Leu Lys Tyr Pro Asn Pro Ser Leu Gln Trp His Tyr Arg Ile Leu
        500             505             510

Gln Ala Leu Ala Leu Asp Glu Asp Leu Pro Glu Lys Pro Glu Asp Lys
        515             520             525

Thr Ile Pro Lys Tyr Arg Gln Ile Asp Lys Arg Ala Gly Asp Tyr Val
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Leu Ser Trp Ala Asp Glu Leu Glu Lys Gln Tyr Ala Lys Thr Ser Ala
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Ala Ala Pro Arg Pro Thr Ser Thr Leu Val Lys Arg Gly Ser Lys Asp
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Arg Ala Ser Glu Thr Glu Asp Ser Lys Pro Ser Lys Lys Ile Lys Val
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Glu Glu Asp Ser Gly Ser Leu Glu Glu Glu Val Arg Arg His His Lys
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Lys Gly Thr Leu Ser Lys Leu Thr Val Ala Ile Leu Lys Asp Phe Leu
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<212> PRT
<213> Aspergillus niger

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Met Gln Tyr Val Trp Asp Arg Ile Thr Gly Thr Val Ala Thr Gly Arg
        35   40   45

Lys Met Ala Leu Ile Gly Val Leu Gly Leu Arg Thr Asp Val Cys Trp
    50   55   60

Ser Gly Leu Met Gln Glu Arg Pro Glu Thr Ala Asn Glu Leu Glu Asp
65   70   75   80

Asp Pro Asp Tyr Ser His Ile Ser Val Leu Ser Gly Ile Lys Gln Phe
                85   90   95

Leu Met Pro Asp Ile Arg Gly Leu Ser Asp Arg Ile Lys Pro Ser Lys
            100   105   110

Thr Asn Lys Gly Asp Ala Ile Ser Ala Leu Val Leu Ala Ile Gln Met
        115   120   125

Ile Ile Thr Gln Cys Lys Lys Leu Lys Tyr Lys Arg Arg Ile Val Leu
    130   135   140

Val Thr Asn Gly Gln Gly Pro Met Asn Pro Asp Asn Leu Ser Glu Ile
145   150   155   160

Thr Lys Lys Ile Lys Glu Asp Asn Ile Glu Leu Ile Ile Leu Gly Pro
                165   170   175

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Arg Lys Ala Glu Asn Glu Thr Leu Leu Arg Ser Leu Ala Glu Asp Cys
        195             200                 205

Glu Gly Ala Tyr Gly Thr Leu Glu Gln Ala Val Ala Glu Leu Glu Thr
    210             215             220

Pro Arg Val Lys Thr Thr Arg Ile Thr Ala Ser Phe Lys Gly His Leu
225             230             235                 240

Gln Leu Gly Asn Pro Ala Glu Tyr Asp Thr Ala Val Arg Ile Pro Val
            245             250                 255

Glu Arg Tyr Tyr Arg Thr Tyr Val Ala Lys Ala Pro Ser Ala Ser Gln
        260             265                 270

Phe Thr Val Arg Asn Glu Glu Glu Met Gly Met Ala Ala Ala Ala Ala
        275             280             285

Gly Ser Gln Glu Gly Ser Ser Leu Val Gly Val Arg Asn Asn Arg Ser
    290             295             300

Tyr Gln Ile Asp Asp Gly Thr Thr Glu Glu Gly Val Arg Asp Val Asp
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Arg Glu Gln Leu Ala Lys Gly Tyr Glu Tyr Gly Arg Thr Leu Val Pro
            325             330                 335

Ile Ser Glu Thr Asp Glu Asn Ile Thr Thr Leu Glu Thr Phe Ala Ala
            340             345             350

Ile Glu Leu Leu Gly Phe Ile Gln Ser Asp Arg Tyr Asp Arg Tyr Met
        355             360             365

His Met Ser Thr Thr Asn Ile Ile Ile Ala Gln Arg Ala Asn Asp Lys
    370             375             380

Ala Ala Leu Ala Leu Ser Ser Phe Ile His Ala Leu Phe Glu Leu Glu
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            420              425              430

Glu Ala Gln Leu Pro Phe Ala Glu Asp Val Arg Thr Tyr Arg Phe Pro
        435              440              445

Pro Leu Asp Arg Val Ile Thr Val Ser Gly Lys Val Val Thr Gln His
    450              455              460

Arg Asn Leu Pro Asn Asp Asp Leu Leu Asn Ala Met Asp Lys Tyr Val
465              470              475              480

Lys Ser Met Glu Leu Thr Asp Met Asp Glu Asn Gly Asp Pro Thr Glu
            485              490              495

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            500              505              510

Ser Ala Ile Arg His Arg Ala Ile His Pro Asn Asp Pro Ile Pro Pro
            515              520              525

Pro Ala Ser Val Leu Thr Lys Phe Ser His Pro Pro Asp Asp Leu Val
    530              535              540

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cctataatag actagcgtgc ttggcattag ggttcgaaaa acaatcgaag agtataaggg      3240
gatgacagca gtaacgactc caactgtagc ccacatcttg agttcggcaa ctactgttgg      3300
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cgtcaagctc cagcagtgct ggggcctcgg ctatgatatg gttagaatgc tcggggtggg      3660
tcacggcagg acacccgaca ctgcaacgtc taccacattt gagcgttatt ggcagacttg      3720
cggcgagata acgaccgcta gcttgtatca accaaatcca actgaaatta ttgctttgcc      3780
atcccaacag tggatttcgg aggaggagg gggaagata tacgatgaac ggaagactgg      3840
acaagatacg ttacataaag cagtactact tgtttcaaac tgtgtacaca ccagggctct      3900
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<210> 10
<211> 1497
<212> DNA
<213> Aspergillus niger

<220>
<221> CDS
<222> (1)..(1497)

<400> 10

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1               5                   10                  15

cct gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat      96
Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
            20                  25                  30

ttc ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg      144
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
        35                  40                  45

act tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc      192
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
    50                  55                  60

atc atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc      240
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65                  70                  75                  80

tgg atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga      288
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
                85                  90                  95

gat gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa      336
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
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                      100                     105                     110
aac tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat          384
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
            115                     120                     125
gag agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc          432
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
        130                     135                     140
tat gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc          480
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145                     150                     155                     160
agt tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa          528
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
                    165                     170                     175
gat cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc          576
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
            180                     185                     190
ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac          624
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
                195                     200                     205
gac tgg gtg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt          672
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
        210                     215                     220
atc gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac          720
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225                     230                     235                     240
aaa gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg          768
Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
                    245                     250                     255
gcc tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat          816
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
                260                     265                     270
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc          864
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
            275                     280                     285
atg gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca          912
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
        290                     295                     300
gac tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg          960
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305                     310                     315                     320
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca          1008
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
                    325                     330                     335
ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa          1056
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
                340                     345                     350
cag cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg          1104
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
            355                     360                     365
ctc tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc          1152
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
        370                     375                     380
gcg aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg          1200
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
385                     390                     395                     400
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg          1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
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                    405                    410                    415
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag          1296
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
            420                    425                    430
ggt gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac          1344
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
            435                    440                    445
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg          1392
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
    450                    455                    460
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct          1440
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465                    470                    475                    480
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt          1488
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
                    485                    490                    495
agc tcg tga                                                              1497
Ser Ser
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<210> 11
<211> 498
<212> PRT
<213> Aspergillus niger

<400> 11
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Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
            20                  25                  30
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
            35                  40                  45
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
    50                  55                  60
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65                  70                  75                  80
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
                85                  90                  95
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
            100                 105                 110
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
            115                 120                 125
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
    130                 135                 140
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145                 150                 155                 160
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
                165                 170                 175
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
            180                 185                 190
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
            195                 200                 205
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
    210                 215                 220
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225                 230                 235                 240
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Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
             245                 250                 255
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
             260                 265                 270
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
             275                 280                 285
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
     290                 295                 300
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305                 310                 315                 320
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
             325                 330                 335
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
             340                 345                 350
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
             355                 360                 365
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
     370                 375                 380
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
385                 390                 395                 400
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
             405                 410                 415
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
             420                 425                 430
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
             435                 440                 445
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
     450                 455                 460
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465                 470                 475                 480
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
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<210> 12
<211> 3697
<212> DNA
<213> Aspergillus niger

<400> 12

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aggttgtgtc tgtataatat atacatgtaa gatacatgag cttcggtgat ataatacaga   180
agtaccatac agtaccgcgt tatgaaaaca cattaatccg gatcctttcc tataatagac   240
tagcgtgctt ggcattaggg ttcgaaaaac aatcgaagag tataagggga tgacagcagt   300
aacgactcca actgtacgcc tccgggtagt agaccgagca gccgagccag ctcagcgcct   360
aaaacgcctt atacaattaa gcagttaaag aagttagaat ctacgcttaa aaagctactt   420
aaaaatcgat ctcgcagtcc cgattcgcct atcaaaacca gtttaaatca actgattaaa   480
ggtgccgaac gagctataaa tgatataaca atattaaagc attaattaga gcaatatcag   540
gccgcgcacg aaaggcaact taaaaagcga aagcgctcta ctaaacagat tacttttgaa   600
aaaggcacat cagtatttaa agcccgaatc cttattaagc gccgaaatca ggcagataaa   660
gccatacagg cagatagacc tctacctatt aaatcggctt ctaggcgcgc tccatctaaa   720
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tcattttttt atatagaagtca gaattcatgg tgttttgatc attttaaatt tttatatggc   840
gggtggtggg caactcgctt cgcgggcaa ctcgcttacc gattacgtta gggctgatat   900
ttacgtaaaa atcgtcaagg gatgcaagac caaagtagta aaacccccgga gtcaacagca   960
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gtcggcccgt cggccttttc tgcaacgctg atcacgggca gcgatccaac caacacccctc   1140
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cgtccccggt attgtcctgc agaatgcaat ttaaactctt ctgcgaatcg cttggattcc    1260
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gatgacttga aggcgctctc ttcggccctt catgagaggg ggatgtatct tatggtcgat    2040
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<210> 13
<211> 1497
<212> DNA
<213> Aspergillus niger

<220>
<221> CDS
<222> (1)..(1497)

<400> 13

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1               5                   10                  15
cct gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat        96
Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
            20                  25                  30
ttc ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg       144
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
        35                  40                  45
act tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc       192
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
    50                  55                  60
atc atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc       240
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65                  70                  75                  80
tgg atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga       288
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
                85                  90                  95
gat gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa       336
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
            100                 105                 110
aac tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat       384
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
        115                 120                 125
gag agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc       432
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
    130                 135                 140
tat gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc       480
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145                 150                 155                 160
agt tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa       528
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
                165                 170                 175
gat cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc       576
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
                180                 185                 190
ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac       624
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
            195                 200                 205
gac tgg gtg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt       672
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
    210                 215                 220
atc gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac       720
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225                 230                 235                 240
aaa gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg       768
Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
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gcc tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat       816
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
            260                 265                 270
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc       864
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
        275                 280                 285
atg gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca       912
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
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305                   310                   315                   320
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca        1008
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
                  325                   330                   335
ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa        1056
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
                  340                   345                   350
cag cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg        1104
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
                  355                   360                   365
ctc tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc        1152
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
                  370                   375                   380
gcg aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg        1200
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
385                   390                   395                   400
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg        1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
                  405                   410                   415
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag        1296
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
                  420                   425                   430
ggt gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac        1344
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
                  435                   440                   445
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg        1392
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
             450                   455                   460
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct        1440
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465                   470                   475                   480
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt        1488
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
                  485                   490                   495
agc tcg tga                                                            1497
Ser Ser
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<210> 14
<211> 498
<212> PRT
<213> Aspergillus niger

<400> 14

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          20                   25                   30
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
          35                   40                   45
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
     50                   55                   60
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
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65                    70                    7 5                    80
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
            85                    90                    95
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
            100                   105                   110
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
            115                   120                   125
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
    130                   135                   140
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145                   150                   155                   160
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
                165                   170                   175
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
            180                   185                   190
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
            195                   200                   205
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
    210                   215                   220
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225                   230                   235                   240
Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
                245                   250                   255
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
            260                   265                   270
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
            275                   280                   285
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
    290                   295                   300
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305                   310                   315                   320
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
                325                   330                   335
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
            340                   345                   350
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
            355                   360                   365
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
    370                   375                   380
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
385                   390                   395                   400
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
                405                   410                   415
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
                420                   425                   430
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
            435                   440                   445
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
    450                   455                   460
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465                   470                   475                   480
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
                485                   490                   495
Ser Ser
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<210> 15

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<211> 3570
<212> DNA
<213> Aspergillus niger

<400> 15
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ataaatgaaa gcacgcatgt atcagcctaa tagccgagtg gcgggcatct ctggcggcct       180
cccgagcagc gtggaatgcg tccaagatcc cgtccgcggg tcgtccttcg gtcggaatga       240
tgactggagc agcagacgat gtcctgagct gaatgcatgt gatattcaca ttccagggag       300
aattgtcggc tatttagaac cctctcggct taaaagccct attagactat gggtgcgctc       360
aagccactag ccaggatatc ccgctgaacg ctccatcacc ttgcagctga agtgcaacat       420
gggacgggct ttaactttc gtagatataa gtttaattta tcctctccac acccataggg       480
tcgtatggtg tcaaccggtg tagtctgcag gatttcatct cgcttcgcca agcgaggcgc       540
cctaacgggc agcctgcagc ttaccctgtt aaccccggct caccacccc cgagcaatcc       600
gtcgcgtcct ccacgagtca taacaaggtt cgggcgttgt ttcttacccc cactatcagg       660
cgtattcagt taacagtcag tagtcccgtg tcggagattt gttgttctgc aacaattaaa       720
ggggaccagg gttaaatcct ggccccgaa ctgatcggag tttcggccaa tgagagatgt       780
tgtataccc cgttcctggc agatggatta attgccggct ccatttggca tccatcaagc       840
atcatacggg attagaaggg tagttcgtgg gttgatctgc cgtgcaaggt gctcaaggct       900
ctggagtcat gctgaacgca aatatttaag aatcgtcgtc agggacagcg ttctctggat       960
agtcaagctg tgcttgggac gctgttctgt cgctttgtca aaacataatt cgcagcgatg      1020
agattatcga cttcgagtct cttcctttcc gtgtctctgc tggggaagct ggccctcggg      1080
ctgtcggctg cagaatggcg cactcagtcg atttacttcc tattgacgga tcggttcggt      1140
aggacggaca attcgacgac agctacatgc gatacgggtg accaagtacg ttggtattgc      1200
aggacttcca tcattcatct actgacttga atagatctat tgtggtggca gttggcaagg      1260
aatcatcaac catgtttgtg atcacttcat actatccgct gtgcgcgtgt ctgactttat      1320
ttgctgcagc tggattatat ccagggcatg ggattcacgg ccatctggat ctcgcctatc      1380
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aagatgtatg cgctcctcct tcccatatcg taggcttact ctcaggcggc gactgacttg      1500
acagatacga cgtgaactcc aacttcggca ctgcagatga cctcaagtcc ctctcagatg      1560
cgcttcatgc ccgcggaatg tacctcatgg tggacgtcgt ccctaaccac atggtaagtg      1620
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tccacccata ctgcctgatc acagattggg acaacttgac catggtccaa gattgttggg      1800
agggtgacac catcgtatct ctgccagacc taaacaccac cgaaactgcc gtgagaacaa      1860
tctggtatga ctgggtagcc gacctggtat ccattattc aggtgcgaat tccaacccaa      1920
tttaaaataa ccatatacta agtgaaatca ccagtcgacg gactccgcat cgacagtgtc      1980
ctcgaagtcg aaccagactt cttcccgggc taccaggaag cagcaggtgt ctactgcgtc      2040
ggcgaagtcg acaacggaa ccctgccctc gactgcccat accagaaggt cctggacggc      2100
gtcctcaact atccgatgta catcccccta tacattgttc attagatctt cgctaactcc      2160
aaccagctac tggcaactcc tctacgcctt cgaatcctcc agcggcagca tcagcaacct      2220
ctacaaacatg atcaaatccg tcgcaagcga ctgctccgat ccgacactac tcggcaactt      2280
catcgaaaac cacgacaatc cccgtttcgc ctcgtatgtc ccaccccctc ccctccctac      2340
aatcacactc actaatacat ctaacagcta cacctccgac tactcgcaag ccaaaaacgt      2400
cctcagctac atcttcctct ccgacggcat ccccatcgtc tacgccggcg aagaacagca      2460
ctactccggc ggcaaggtgc cctacaaccg cgaagcgacc tggctttcag gctacgacac      2520
ctccgcagag ctgtacacct ggatagccac cacgaacgcg atccgcaaac tagccatctc      2580
agctgactcg gcctacatta cctacgcggt tcgtccttcc ctcccaccct taccccca      2640
ccctacaaac atcccacata ctaacaacat ttcaataatg aaatagaatg atgcattcta      2700
cactgacagc aacaccatcg caatgcgcaa aggcacctca gggagccaag tcatcaccgt      2760
cctctccaac aaaggctcct caggaagcag ctacaccctg accctcagcg gaagcggcta      2820
cacatccggc acgaagctga tcgaagcgta cacatgcaca tccgtgaccg tggactcgag      2880
cggcgatatt cccgtgccga tggcgtcggg attaccgaga gttcttctgc ccgcgtccgt      2940
cgtcgatagc tcttcgctct gtggcgggag cggaagatta tacgtcgagt aatccggagt      3000
ggtcggttac tgtgacgttg ccggtgggga ccactttcga gtataagttt attaaggtgg      3060
agtcggatgg gactgttact tgggaaagtg attcgaatcg ggagtatacg gtgccggagt      3120
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gtgggagtgg ggagacggtg gttgatactt ggaggtagat gatctgagat ttctaagtgt   3180
gatgagggtg gtttttggtgt atgtagtttg gcctttggta gtgttgggtt gggttggggtt  3240
aataattatg ttattgtttt tggtgcttgt gaccatggat ttgaagtgaa aatttgtagg   3300
ggctacggaa gtgtattgtg gacatgtgag taaattcatc tgggtatgta caaagtgggt   3360
tagccagtgg gcttgaagaa aagtctcctg ggtctctggt ttgagtaccc atgttaagat   3420
caagcataaa aacatgaaat attgggaaaa caaagggtat ttaacaactc gtgagcatta   3480
gctcctgggt agaatgcaat cataacagaa agtacagcca gcgctgtgtc ataaagaagt   3540
ccagttggga aacgaaagac tagaatcaaa                                     3570
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<210> 16
<211> 1518
<212> DNA
<213> Aspergillus niger

<220>
<221> CDS
<222> (1)..(1518)

<400> 16

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Met Arg Leu Ser Thr Ser Ser Leu Phe Leu Ser Val Ser Leu Leu Gly
1               5                   10                  15
aag ctg gcc ctc ggg ctg tcg gct gca gaa tgg cgc act cag tcg att    96
Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile
            20                  25                  30
tac ttc cta ttg acg gat cgg ttc ggt agg acg gac aat tcg acg aca    144
Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
        35                  40                  45
gct aca tgc gat acg ggt gac caa atc tat tgt ggt ggc agt tgg caa    192
Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
    50                  55                  60
gga atc atc aac cat ctg gat tat atc cag ggc atg gga ttc acg gcc    240
Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
65                  70                  75                  80
atc tgg atc tcg cct atc act gaa cag ctg ccc cag gat act gct gat    288
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp
                85                  90                  95
ggt gaa gct tac cat gga tat tgg cag cag aag ata tac gac gtg aac    336
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn
            100                 105                 110
tcc aac ttc ggc act gca gat gac ctc aag tcc ctc tca gat gcg ctt    384
Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
        115                 120                 125
cat gcc cgc gga atg tac ctc atg gtg gac gtc gtc cct aac cac atg    432
His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
    130                 135                 140
ggc tac gcc ggc aac ggc aac gat gta gac tac agc gtc ttc gac ccc    480
Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
145                 150                 155                 160
ttc gat tcc tcc tcc tac ttc cac cca tac tgc ctg atc aca gat tgg    528
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
                165                 170                 175
gac aac ttg acc atg gtc caa gat tgt tgg gag ggt gac acc atc gta    576
Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
            180                 185                 190
tct ctg cca gac cta aac acc acc gaa act gcc gtg aga aca atc tgg    624
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Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp
    195                 200                 205
tat gac tgg gta gcc gac ctg gta tcc aat tat tca gtc gac gga ctc      672
Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
    210                 215                 220
cgc atc gac agt gtc ctc gaa gtc gaa cca gac ttc ttc ccg ggc tac      720
Arg Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
225                 230                 235                 240
cag gaa gca gca ggt gtc tac tgc gtc ggc gaa gtc gac aac ggc aac      768
Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
                245                 250                 255
cct gcc ctc gac tgc cca tac cag aag gtc ctg gac ggc gtc ctc aac      816
Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn
            260                 265                 270
tat ccg atc tac tgg caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc      864
Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
        275                 280                 285
agc atc agc aac ctc tac aac atg atc aaa tcc gtc gca agc gac tgc      912
Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
    290                 295                 300
tcc gat ccg aca cta ctc ggc aac ttc atc gaa aac cac gac aat ccc      960
Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
305                 310                 315                 320
cgt ttc gcc tcc tac acc tcc gac tac tcg caa gcc aaa aac gtc ctc     1008
Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
                325                 330                 335
agc tac atc ttc ctc tcc gac ggc atc ccc atc gtc tac gcc ggc gaa     1056
Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
            340                 345                 350
gaa cag cac tac tcc ggc ggc aag gtg ccc tac aac cgc gaa gcg acc     1104
Glu Gln His Tyr Ser Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr
        355                 360                 365
tgg ctt tca ggc tac gac acc tcc gca gag ctg tac acc tgg ata gcc     1152
Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala
    370                 375                 380
acc acg aac gcg atc cgc aaa cta gcc atc tca gct gac tcg gcc tac     1200
Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr
385                 390                 395                 400
att acc tac gcg aat gat gca ttc tac act gac agc aac acc atc gca     1248
Ile Thr Tyr Ala Asn Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala
                405                 410                 415
atg cgc aaa ggc acc tca ggg agc caa gtc atc acc gtc ctc tcc aac     1296
Met Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn
            420                 425                 430
aaa ggc tcc tca gga agc agc tac acc ctg acc ctc agc gga agc ggc     1344
Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly
        435                 440                 445
tac aca tcc ggc acg aag ctg atc gaa gcg tac aca tgc aca tcc gtg     1392
Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val
    450                 455                 460
acc gtg gac tcg agc ggc gat att ccc gtg ccg atg gcg tcg gga tta     1440
Thr Val Asp Ser Ser Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu
465                 470                 475                 480
ccg aga gtt ctt ctg ccc gcg tcc gtc gtc gat agc tct tcg ctc tgt     1488
Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys
                485                 490                 495
ggc ggg agc gga aga tta tac gtc gag taa                             1518
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Gly Gly Ser Gly Arg Leu Tyr Val Glu
        500                     505


<210> 17
<211> 505
<212> PRT
<213> Aspergillus niger

<400> 17
Met Arg Leu Ser Thr Ser Ser Leu Phe Leu Ser Val Ser Leu Leu Gly
1               5                   10                  15
Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile
            20                  25                  30
Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
            35                  40                  45
Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
    50                  55                  60
Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
65                  70                  75                  80
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp
                85                  90                  95
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn
            100                 105                 110
Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
        115                 120                 125
His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
    130                 135                 140
Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
145                 150                 155                 160
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
                165                 170                 175
Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
            180                 185                 190
Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp
        195                 200                 205
Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
    210                 215                 220
Arg Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
225                 230                 235                 240
Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
                245                 250                 255
Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn
            260                 265                 270
Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
    275                 280                 285
Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
    290                 295                 300
Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
305                 310                 315                 320
Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
                325                 330                 335
Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
            340                 345                 350
Glu Gln His Tyr Ser Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr
        355                 360                 365
Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala
```

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      370                      375                      380
Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr
385                      390                      395                      400


Ile Thr Tyr Ala Asn Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala
                405                      410                      415
Met Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn
                420                      425                      430
Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly
                435                      440                      445
Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val
                450                      455                      460
Thr Val Asp Ser Ser Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu
465                      470                      475                      480
Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys
                485                      490                      495
Gly Gly Ser Gly Arg Leu Tyr Val Glu
                500                      505
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<210> 18
<211> 2935
<212> DNA
<213> Penicillium chrysogenum

<400> 18

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atgaagagat gacaattccg acttccaact tccaacttgg acctcggagt tgttgaatcc   120
ggtcctgctt gccccatata gcttccgacc accggatttg gaccaatcaa cgcaggaaga   180
tgtcagcagc ttcaggcatc agcgtcacct gaccttcgtg ttgcccgcgt caacgagcgc   240
gtctcaatga tactttagac ttgattaatt tacacctttt aatatttcca atctcccgag   300
gatacctact tcgtaacaat ggttgaagat agctacacgc gcgaggagga gaattacgag   360
gatgaagagc tcgacgagac cgtgagtatc aaaagttgga gatatagtta ccgattgttg   420
acggttgcct acatagagct tcaaatcagt caaagatgcg gtgctgtttg ctatagatat   480
tagcagttcg atgctcacgc ctcgtccatc gcctgatcct aagaaacatg gagacgaatc   540
acccgcgtct gcagctttga agtgtgcata ccatctgatg caacaacgca tcatctccaa   600
ccctcatgac atgattggcg ttttgcttta cggaacgcaa tcttccaagt tctatgatga   660
aaatgaggat gaccgtggag atctctcata tcctcactgt tatctgtaca cggatcttga   720
tgttccatca gcccaggaag tcaagcaact gcggtccctc gcatctccag cagatgctga   780
tgatgacgta ctgcaagttt tggagccatc aaaggagcca gcctccatgg ccaacatgct   840
tttctgcgcc aaccaaatct ttacctcaaa agctccaaac tttgcttctc gacgcctgtt   900
tgtcgtgacc gacaacgata tcccccacgc agacaacaaa ggaatgcggt ctgctgcaac   960
agttcgtgcg agggacttgt acgatcttgg tgtcaatatc gagttgtttc ccatatctca  1020
accagaccac gaattcgaca cctctaaatt ctacgacgta ggtcattaac cttgattgca  1080
taggggtata ctcacaattg gcaggacatt atctacaaaa catcgcccag tgatggagat  1140
gcccctgcat acctacagcc ggataccaac acatcaacag ctaaaggcga tggactttca  1200
ttgctcaatt ctctgttgtc gagcatcaac tcacgatctg tccccgccg atcgctgttc   1260
tcaaatgtgc cacttgagat cggacctaat ttcaaaatat ccgtcaatgg atatttgctt  1320
ctcaagaaac aagagcctgc aaggagttgc ttcgtctggc aaggaggcga gactgctcag  1380
attgccaaag gagtcacaac tctaatgtct gatgacacag ggcaggagat tgagaagtct  1440
gacattcgca aggcatacaa gtttggtggc gagcaggtat cattcaccat cgaagaacaa  1500
caggcgctaa gaagcttcgg tgacccggtg atccgtatta ttgggttcaa gccactgtca  1560
gccctcccgt tctgggccaa tgtcaagcac ccctcgttta tttatccctc tgaagaggac  1620
tacgtcggtt caacaagagt cttttctgca ctgcatcaga aactcctcga atcggagaaa  1680
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ctggctttgg tctggttcat cccccgcaga aatgcctcac cagtcttagc tgctatgatt    1740
gcaggtgctg agaagatcga cgagaatggc gtgcagaaaa ttccacctgg gatgtggatt    1800
atccctcttc ctttcgcaga tgatgtgcgc caaaatccag agagcaccgt ccaccgggca    1860
ggagatgcgc tgaacgacgc catgcgagat gttgttcgcc agttgcagct ccccaaggct    1920
gtgtacgatc cttcaaaata tccgaatcct tgtgagcctt cgtcacttca atctttggga    1980
caatgatact gactgattcg cagcgcttca atggcattat cgtatcttac aggctatcgc    2040
cttggatgaa gatttcccag aatcaccaga tgacaagacc gtgcctaagt accgacaggt    2100
tcacaaggtt ggctgcttcc atgatcccag aaatgcccga acgtactgac caaatggatg    2160
ttctagcgcg ctggcgacta tattcttaga tgggccgagg aactgaaatt gcaagcctcc    2220
gagatgtttg gtgggtcagt agccgccacc tctacgctgg taaagcgagg tgccaagacc    2280
gaggcagctg gtgagcaccc atcaaagcgg gtgaaggttg aagacagtga gcccggagtg    2340
gaagacgaag tgaagaaatg ctatgcgaaa ggcactgttt ccaaggtgag cattcaaatt    2400
ctccaggtg attgaccaaa ctaatactcg ccttcagctt acggtggccg tgctgaagga    2460
attcttgcat gcacatggcc gtgctacagc aggaaagaaa gcagatctcg tggaccgagt    2520
tgagcagtac tttgagcaga agttttaaac attgatttga agtttgctca ggatcgtctt    2580
ggggtggtcc aaggttgctg taatctgcgg cccgtttaat gagttatgag tgtatcctac    2640
ttgcctgttt ccataaggtc atagtcattt caaatgaatc gatatctttt atccaggatg    2700
atgttaggga cattatatat aagaatatac cggcgtttct ttttcgatgt cttttcagat    2760
gtatacaaag gcgcaagccg gtaaaaggcg tgaacgccct gatatatatc accgatactt    2820
ctttatgcaa aatgccagaa aatacctcta gcaactacag gggtagaaaa agagatcacc    2880
cttccaaggt tggcctagtc ttcctagata gccttctccg atagtcactt catac          2935
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<210>  19
<211>  1977
<212>  DNA
<213>  Penicillium chrysogenum

<220>
<221>  CDS
<222>  (1)..(1977)

<400>  19
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atg gtt gaa gat agc tac acg cgc gag gag gag aat tac gag gat gaa      48
Met Val Glu Asp Ser Tyr Thr Arg Glu Glu Glu Asn Tyr Glu Asp Glu
1               5                   10                  15
gag ctc gac gag acc agc ttc aaa tca gtc aaa gat gcg gtg ctg ttt     96
Glu Leu Asp Glu Thr Ser Phe Lys Ser Val Lys Asp Ala Val Leu Phe
                20                  25                  30
gct ata gat att agc agt tcg atg ctc acg cct cgt cca tcg cct gat     144
Ala Ile Asp Ile Ser Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp
            35                  40                  45
cct aag aaa cat gga gac gaa tca ccc gcg tct gca gct ttg aag tgt     192
Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys
        50                  55                  60
gca tac cat ctg atg caa caa cgc atc atc tcc aac cct cat gac atg     240
Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met
65                  70                  75                  80
att ggc gtt ttg ctt tac gga acg caa tct tcc aag ttc tat gat gaa     288
Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu
                85                  90                  95
aat gag gat gac cgt gga gat ctc tca tat cct cac tgt tat ctg tac     336
Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
                100                 105                 110
acg gat ctt gat gtt cca tca gcc cag gaa gtc aag caa ctg cgg tcc     384
Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
            115                 120                 125
```

```
ctc gca tct cca gca gat gct gat gat gac gta ctg caa gtt ttg gag        432
Leu Ala Ser Pro Ala Asp Ala Asp Asp Asp Val Leu Gln Val Leu Glu
    130             135             140
cca tca aag gag cca gcc tcc atg gcc aac atg ctt ttc tgc gcc aac        480
Pro Ser Lys Glu Pro Ala Ser Met Ala Asn Met Leu Phe Cys Ala Asn
145             150             155                 160
caa atc ttt acc tca aaa gct cca aac ttt gct tct cga cgc ctg ttt        528
Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe
            165             170             175
gtc gtg acc gac aac gat aat ccc cac gca gac aac aaa gga atg cgg        576
Val Val Thr Asp Asn Asp Asn Pro His Ala Asp Asn Lys Gly Met Arg
            180             185                 190
tct gct gca aca gtt cgt gcg agg gac ttg tac gat ctt ggt gtc aat        624
Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn
    195             200             205
atc gag ttg ttt ccc ata tct caa cca gac cac gaa ttc gac acc tct        672
Ile Glu Leu Phe Pro Ile Ser Gln Pro Asp His Glu Phe Asp Thr Ser
    210             215             220
aaa ttc tac gac gac att atc tac aaa aca tcg ccc agt gat gga gat        720
Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp
225             230             235                 240
gcc cct gca tac cta cag ccg gat acc aac aca tca aca gct aaa ggc        768
Ala Pro Ala Tyr Leu Gln Pro Asp Thr Asn Thr Ser Thr Ala Lys Gly
            245             250             255
gat gga ctt tca ttg ctc aat tct ctg ttg tcg agc atc aac tca cga        816
Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg
            260             265             270
tct gtc ccc cgc cga tcg ctg ttc tca aat gtg cca ctt gag atc gga        864
Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly
    275             280             285
cct aat ttc aaa ata tcc gtc aat gga tat ttg ctt ctc aag aaa caa        912
Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Leu Lys Lys Gln
    290             295             300
gag cct gca agg agt tgc ttc gtc tgg caa gga ggc gag act gct cag        960
Glu Pro Ala Arg Ser Cys Phe Val Trp Gln Gly Gly Glu Thr Ala Gln
305             310             315                 320
att gcc aaa gga gtc aca act cta atg tct gat gac aca ggg cag gag       1008
Ile Ala Lys Gly Val Thr Thr Leu Met Ser Asp Asp Thr Gly Gln Glu
            325             330             335
att gag aag tct gac att cgc aag gca tac aag ttt ggt ggc gag cag       1056
Ile Glu Lys Ser Asp Ile Arg Lys Ala Tyr Lys Phe Gly Gly Glu Gln
            340             345             350
gta tca ttc acc atc gaa gaa caa cag gcg cta aga agc ttc ggt gac       1104
Val Ser Phe Thr Ile Glu Glu Gln Gln Ala Leu Arg Ser Phe Gly Asp
            355             360             365
ccg gtg atc cgt att att ggg ttc aag cca ctg tca gcc ctc ccg ttc       1152
Pro Val Ile Arg Ile Ile Gly Phe Lys Pro Leu Ser Ala Leu Pro Phe
    370             375             380
tgg gcc aat gtc aag cac ccc tcg ttt att tat ccc tct gaa gag gac       1200
Trp Ala Asn Val Lys His Pro Ser Phe Ile Tyr Pro Ser Glu Glu Asp
385             390             395                 400
tac gtc ggt tca aca aga gtc ttt tct gca ctg cat cag aaa ctc ctc       1248
Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu
            405             410             415
gaa tcg gag aaa ctg gct ttg gtc tgg ttc atc ccc cgc aga aat gcc       1296
Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala
            420             425             430
```

```
tca cca gtc tta gct gct atg att gca ggt gct gag aag atc gac gag        1344
Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu
        435                 440                 445
aat ggc gtg cag aaa att cca cct ggg atg tgg att atc cct ctt cct        1392
Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro
        450                 455                 460
ttc gca gat gat gtg cgc caa aat cca gag agc acc gtc cac cgg gca        1440
Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala
465                 470                 475                 480
gga gat gcg ctg aac gac gcc atg cga gat gtt gtt cgc cag ttg cag        1488
Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln
        485                 490                 495
ctc ccc aag gct gtg tac gat cct tca aaa tat ccg aat cct tcg ctt        1536
Leu Pro Lys Ala Val Tyr Asp Pro Ser Lys Tyr Pro Asn Pro Ser Leu
        500                 505                 510
caa tgg cat tat cgt atc tta cag gct atc gcc ttg gat gaa gat ttc        1584
Gln Trp His Tyr Arg Ile Leu Gln Ala Ile Ala Leu Asp Glu Asp Phe
        515                 520                 525
cca gaa tca cca gat gac aag acc gtg cct aag tac cga cag gtt cac        1632
Pro Glu Ser Pro Asp Asp Lys Thr Val Pro Lys Tyr Arg Gln Val His
        530                 535                 540
aag gtt ggc tgc ttc cat gat ccc aga aat gcc cga aca tgg gcc gag        1680
Lys Val Gly Cys Phe His Asp Pro Arg Asn Ala Arg Thr Trp Ala Glu
545                 550                 555                 560
gaa ctg aaa ttg caa gcc tcc gag atg ttt ggt ggg tca gta gcc gcc        1728
Glu Leu Lys Leu Gln Ala Ser Glu Met Phe Gly Gly Ser Val Ala Ala
        565                 570                 575
acc tct acg ctg gta aag cga ggt gcc aag acc gag gca gct ggt gag        1776
Thr Ser Thr Leu Val Lys Arg Gly Ala Lys Thr Glu Ala Ala Gly Glu
        580                 585                 590
cac cca tca aag cgg gtg aag gtt gaa gac agt gag ccc gga gtg gaa        1824
His Pro Ser Lys Arg Val Lys Val Glu Asp Ser Glu Pro Gly Val Glu
        595                 600                 605
gac gaa gtg aag aaa tgc tat gcg aaa ggc act gtt tcc aag ctt acg        1872
Asp Glu Val Lys Lys Cys Tyr Ala Lys Gly Thr Val Ser Lys Leu Thr
        610                 615                 620
gtg gcc gtg ctg aag gaa ttc ttg cat gca cat ggc cgt gct aca gca        1920
Val Ala Val Leu Lys Glu Phe Leu His Ala His Gly Arg Ala Thr Ala
625                 630                 635                 640
gga aag aaa gca gat ctc gtg gac cga gtt gag cag tac ttt gag cag        1968
Gly Lys Lys Ala Asp Leu Val Asp Arg Val Glu Gln Tyr Phe Glu Gln
        645                 650                 655
aag ttt taa                                                            1977
Lys Phe
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<210> 20
<211> 658
<212> PRT
<213> Penicillium chrysogenum

<400> 20

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Met Val Glu Asp Ser Tyr Thr Arg Glu Glu Glu Asn Tyr Glu Asp Glu
1               5                   10                  15
Glu Leu Asp Glu Thr Ser Phe Lys Ser Val Lys Asp Ala Val Leu Phe
            20                  25                  30
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```
Ala Ile Asp Ile Ser Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp
    35                      40                  45
Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys
    50                  55                  60
Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met
65                  70                  75                  80
Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu
                85                  90                  95
Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
            100                 105                 110
Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
        115                 120                 125
Leu Ala Ser Pro Ala Asp Ala Asp Asp Asp Val Leu Gln Val Leu Glu
    130                 135                 140
Pro Ser Lys Glu Pro Ala Ser Met Ala Asn Met Leu Phe Cys Ala Asn
145                 150                 155                 160
Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe
                165                 170                 175
Val Val Thr Asp Asn Asp Asn Pro His Ala Asp Asn Lys Gly Met Arg
            180                 185                 190
Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn
        195                 200                 205
Ile Glu Leu Phe Pro Ile Ser Gln Pro Asp His Glu Phe Asp Thr Ser
    210                 215                 220
Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp
225                 230                 235                 240
Ala Pro Ala Tyr Leu Gln Pro Asp Thr Asn Thr Ser Thr Ala Lys Gly
            245                 250                 255
Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg
            260                 265                 270
Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly
        275                 280                 285
Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Leu Lys Lys Gln
    290                 295                 300
Glu Pro Ala Arg Ser Cys Phe Val Trp Gln Gly Gly Glu Thr Ala Gln
305                 310                 315                 320
Ile Ala Lys Gly Val Thr Thr Leu Met Ser Asp Asp Thr Gly Gln Glu
            325                 330                 335
Ile Glu Lys Ser Asp Ile Arg Lys Ala Tyr Lys Phe Gly Gly Glu Gln
            340                 345                 350
Val Ser Phe Thr Ile Glu Glu Gln Gln Ala Leu Arg Ser Phe Gly Asp
        355                 360                 365
Pro Val Ile Arg Ile Ile Gly Phe Lys Pro Leu Ser Ala Leu Pro Phe
    370                 375                 380
Trp Ala Asn Val Lys His Pro Ser Phe Ile Tyr Pro Ser Glu Glu Asp
385                 390                 395                 400
Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu
                405                 410                 415
Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala
            420                 425                 430
Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu
        435                 440                 445
Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro
    450                 455                 460
Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala
465                 470                 475                 480
Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln
```

```
                   485                    490                    495
Leu Pro Lys Ala Val Tyr Asp Pro Ser Lys Tyr Pro Asn Pro Ser Leu
            500                    505                    510
Gln Trp His Tyr Arg Ile Leu Gln Ala Ile Ala Leu Asp Glu Asp Phe
        515                    520                    525
Pro Glu Ser Pro Asp Asp Lys Thr Val Pro Lys Tyr Arg Gln Val His
        530                    535                    540
Lys Val Gly Cys Phe His Asp Pro Arg Asn Ala Arg Thr Trp Ala Glu
545                    550                    555                    560
Glu Leu Lys Leu Gln Ala Ser Glu Met Phe Gly Gly Ser Val Ala Ala
                565                    570                    575
Thr Ser Thr Leu Val Lys Arg Gly Ala Lys Thr Glu Ala Ala Gly Glu
            580                    585                    590
His Pro Ser Lys Arg Val Lys Val Glu Asp Ser Glu Pro Gly Val Glu
        595                    600                    605
Asp Glu Val Lys Lys Cys Tyr Ala Lys Gly Thr Val Ser Lys Leu Thr
    610                    615                    620
Val Ala Val Leu Lys Glu Phe Leu His Ala His Gly Arg Ala Thr Ala
625                    630                    635                    640
Gly Lys Lys Ala Asp Leu Val Asp Arg Val Glu Gln Tyr Phe Glu Gln
                645                    650                    655
Lys Phe
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<210> 21
<211> 3605
<212> DNA
<213> Penicillium chrysogenum

<400> 21
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gcatcgaggg gaagaagtgg cagttatcgc tacgatccaa ttcttaatga aagccttatt       120
tccacttcca aatagaggga gctggcttct aacgacgcac agaccaccaa acaccaacaa       180
agacggcgtg tgatgtcatg tgccttcgtg tttcggtcta aaccgcaagt ggaaatatca       240
cgcgtctgcc tgttgtcttg agccccaaag caactttgtc ttgccatttt ccacacatca       300
tcatcattat ggcggagaaa gaggctacag tttacattgt agacatggga cggtctatgg       360
gcgagcgcca ccatggccgt cctatgacag atctcgaatg ggccatgcag tatgtctggg       420
ataggatcac tgccacggta tgtgacttga ccttgttcaa cgccagagaa ctgacaattc       480
caggtggcta ctggtcgaaa gacggctacg gttggcgtag ttggactcag gactgatggt       540
gagtggtcgg ctaccagtca gcacccattg ggacccttgt ctcatgtttg gaacaggaac       600
tatcaacgac ttggaagaag agagcttttc taatatttct attctcttcg gtcttggcca       660
gtatgtgtgg cttaattaat cgacagcttt atgccgagtc gcctgactaa attgtctttc       720
agagtcctca tgcctgatat ccggaaactg cgagaaacga tcaagcccag caacactaac       780
agaggcgatg gtatgtgact gttgaagtct tgtcaagctg cttattctga ctttatataa       840
gccatctctt ctattgtcat tgccatgcag atgatcattg actacacgaa gaaaaacaaa       900
tacaagcgca agatcatctt ggtgaccaat ggtaccggcg tgatgagcga tgataatatc       960
gaaggcatca ttgaaaagat gaaagaggtt aacattgagt tggtggtcat gtatgtttct      1020
tgccgacatg acttcacatt catgctaata ctatgcagtg gagccgattt tgatgacgct      1080
gagtatggtg taaaggaaga agacaaagac agtcgaaagg ttctaagcca tctccaatct      1140
attctgttat tcatgttgac aaagcgctct gcaggctgaa aacgagactt ttctccgaag      1200
cctggctgag gactgcgaag gtgcttatgg aacgctggag caagccgttt cggaattgga      1260
tattccccgt atcaaagtga ccaagagcat gccatctttc aagggaaacc tcacgctcgg      1320
caatcccgag gagtatgaca cggctatgac tatacccgtg gagcgatact tccgaaccta      1380
cgtcgccaaa ccaatctcag cgagctcgtt cgtaccacgc tccggcaccg aacctggaag      1440
tcaagcaccg gttaaaggcg atgctgaagg cgatgctctc gcctcagtgc gaacatcacg      1500
gacgtatcag atcacagatg agtccgcacc aggtggtaag atcgacgttg aacgcgatga      1560
cctcgccaag gggtacgagt acggacgtac cgcggttcct atcgagcaaa ccgatgagaa      1620
```

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tgttgcaaat ctacaaacat ttgctggtat ggggctgatc gggttcgttc agaaggatca      1680
ggtgtgtctt tatgccaata ttaagtgcta taacagctaa tccgtgactt agtatgaccg      1740
gtacatgcat atgtcaaaca cgaatatcat catccctcag cgtgcaaatg actatgcgtc      1800
tcttgcgttg tcttctctca ttcatgcact ctacgaattg gagtcctatg cggttgcccg      1860
cttggtgacc aaagaatcca aaccaccgat gcttgtgttg ctagctccat ctatcgaggc      1920
agactatgag tgcttgattg aagtacagct tccatttgca gaagacgtgc ggtcgtatcg      1980
gttcccacct ttggataaga ttatcactgt ctctggcaag gtggtgactg aacatcgaaa      2040
cctcccaagc gtggcgttga agatgcgat gagtaactac gtggacagca tggatttttgt      2100
caccacaaac gacgaagggt aagtatagtc tacttgatta tcgactttat cagttaatca      2160
aaagagccag gcaagccact gacgatctcc caatcgacga gtcattctca ccgttattgc      2220
accgcatcga atcagcagtt cgatatcgtg ctgtgcatcc caatgaccct gtcctcgacc      2280
cctcagagcg gctcactgaa ttcgcacacc cctcagaaga catggtcaag aactccaaat      2340
cccatcttga gaaattgatg tccatagcag atgtcaagaa aggtaacctc gatttccata      2400
ctacatccgg aagataccct actcacccac gcattttgtc ttatagttcc accgaagaca      2460
aaggccgta aacgccaacg tgaaacagag aaacctctct caggtttgga cgtggacgcc      2520
ctgctcagcc tcgaacccaa gcgaacgaag atttccaccg agaatgcaat cccagagttc      2580
aagcaaacac tttcccgcgc ggaaaacatc gacgcaatcc acgacgctgt gcagcagatg      2640
gctaaaatca tcgagagcca gatcacacac agcctcggtc attcaaatta cgaccgtgtt      2700
atcgagggc ttggtactat gcgtgaagaa ctggtggact atgaggaacc ggcggtgtac      2760
aatgactttg tgcgtcagtt gaagggcaag atgttgcggg aggagctggg tggggatcgg      2820
agggagctgt ggtggtttgt aaggaaggga aagcttgggc tcattggcaa gagtgaggtg      2880
gatagctcag ga gcaagaggct caagaggtga ggtttggcct tttattgtgg      2940
aatggaacga gtgctaacac tgcgtatagt ttctggctcc caattgagga attgagtggg      3000
ggggcgggtt attgtctcgc tattcaaaca tgaaatagtg agcatacgag ggatgtggaa      3060
tattcatact attctctatg ccagatttac gcgatgtaga gcttcctgtg gaagttatgt      3120
tatatggtac gtcgtagaag taaggccggg aaacggagta tagtccacct caggtgatga      3180
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ggaaatattg agcaagccca tgaacagcat tgtcatatag acgtagaatg gacacataca      3300
ggaacgaagc ccgcagacag aacaatatga ggcacgaagt gaatcggtgc ccaattgcaa      3360
ggcatgacga gtcgtcaatg aacaacagaa ccaaacgccg tgcataacat gcccaataac      3420
cagtattcgc tccagaaaac agcaaaagac cgagatttgc aaactcaaac attaaaaagc      3480
atccagatgc atcagggaaa aggggtatgc agaagtgttg tcccggtagg acgagaagaa      3540
tggaacaaga agcgctccga ggaaacttgg agagtttcga ggggcgaaag aagagagcag      3600
aacat                                                                   3605
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<210> 22
<211> 2157
<212> DNA
<213> Penicillium chrysogenum

<220>
<221> CDS
<222> (1)..(2157)

<400> 22
atg gcg gag aaa gag gct aca gtt tac att gta gac atg gga cgg tct         48
Met Ala Glu Lys Glu Ala Thr Val Tyr Ile Val Asp Met Gly Arg Ser
1               5                   10                  15
atg ggc gag cgc cac cat ggc cgt cct atg aca gat ctc gaa tgg gcc         96
Met Gly Glu Arg His His Gly Arg Pro Met Thr Asp Leu Glu Trp Ala
                20                  25                  30
atg cag tat gtc tgg gat agg atc act gcc acg gtg gct act ggt cga        144
Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg
            35                  40                  45
aag acg gct acg gtt ggc gta gtt gga ctc agg act gat gtc agc acc        192
Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr
```

```
            50                  55                  60
cat tgg gac cct tgt ctc atg ttt gga aca gga act atc aac gac ttg      240
His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu
65                  70                  75                  80
gaa gaa gag agc ttt tct aat att tct att ctc ttc ggt ctt ggc caa      288
Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln
                    85                  90                  95
gtc ctc atg cct gat atc cgg aaa ctg cga gaa acg atc aag ccc agc      336
Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser
                100                 105                 110
aac act aac aga ggc gat gcc atc tct tct att gtc att gcc atg cag      384
Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln
            115                 120                 125
atg atc att gac tac acg aag aaa aac aaa tac aag cgc aag atc atc      432
Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile
        130                 135                 140
ttg gtg acc aat ggt acc ggc gtg atg agc gat gat aat atc gaa ggc      480
Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly
145                 150                 155                 160
atc att gaa aag atg aaa gag gtt aac att gag ttg gtg gtc atg tat      528
Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr
                165                 170                 175
tat ggt gta aag gaa gaa gac aaa gac agt cga aag gct gaa aac gag      576
Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu
            180                 185                 190
act ttt ctc cga agc ctg gct gag gac tgc gaa ggt gct tat gga acg      624
Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr
        195                 200                 205
ctg gag caa gcc gtt tcg gaa ttg gat att ccc cgt atc aaa gtg acc      672
Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr
        210                 215                 220
aag agc atg cca tct ttc aag gga aac ctc acg ctc ggc aat ccc gag      720
Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu
225                 230                 235                 240
gag tat gac acg gct atg act ata ccc gtg gag cga tac ttc cga acc      768
Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr
                245                 250                 255
tac gtc gcc aaa cca atc tca gcg agc tcg ttc gta cca cgc tcc ggc      816
Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly
                260                 265                 270
acc gaa cct gga agt caa gca ccg gtt aaa ggc gat gct gaa ggc gat      864
Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp
            275                 280                 285
gct ctc gcc tca gtg cga aca tca cgg acg tat cag atc aca gat gag      912
Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu
        290                 295                 300
tcc gca cca ggt ggt aag atc gac gtt gaa cgc gac gac ctc gcc aag      960
Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys
305                 310                 315                 320
ggg tac gag tac gga cgt acc gcg gtt cct atc gag caa acc gat gag     1008
Gly Tyr Glu Tyr Gly Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu
                325                 330                 335
aat gtt gca aat cta caa aca ttt gct ggt atg ggg ctg atc ggg ttc     1056
Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe
            340                 345                 350
gtt cag aag gat cag tat gac cgg tac atg cat atg tca aac acg aat     1104
Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn
```

```
               355                    360                    365
atc atc atc cct cag cgt gca aat gac tat gcg tct ctt gcg ttg tct        1152
Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser
         370                    375                    380
tct ctc att cat gca ctc tac gaa ttg gag tcc tat gcg gtt gcc cgc        1200
Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg
385                    390                    395                    400
ttg gtg acc aaa gaa tcc aaa cca ccg atg ctt gtg ttg cta gct cca        1248
Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro
                   405                    410'                   415
tct atc gag gca gac tat gag tgc ttg att gaa gta cag ctt cca ttt        1296
Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe
              420                    425                    430
gca gaa gac gtg cgg tcg tat cgg ttc cca cct ttg gat aag att atc        1344
Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile
              435                    440                    445
act gtc tct ggc aag gtg gtg act gaa cat cga aac ctc cca agc gtg        1392
Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val
         450                    455                    460
gcg ttg aaa gat gcg atg agt aac tac gtg gac agc atg gat ttt gtc        1440
Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val
465                    470                    475                    480
acc aca aac gac gaa ggg caa gcc act gac gat ctc cca atc gac gag        1488
Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu
                   485                    490                    495
tca ttc tca ccg tta ttg cac cgc atc gaa tca gca gtt cga tat cgt        1536
Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg
              500                    505                    510
gct gtg cat ccc aat gac cct gtc ctc gac ccc tca gag cgg ctc act        1584
Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr
              515                    520                    525
gaa ttc gca cac ccc tca gaa gac atg gtc aag aac tcc aaa tcc cat        1632
Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His
         530                    535                    540
ctt gag aaa ttg atg tcc ata gca gat gtc aag aaa gtt cca ccg aag        1680
Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys
545                    550                    555                    560
aca aaa ggc cgt aaa cgc caa cgt gaa aca gag aaa cct ctc tca ggt        1728
Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly
                   565                    570                    575
ttg gac gtg gac gcc ctg ctc agc ctc gaa ccc aag cga acg aag att        1776
Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile
              580                    585                    590
tcc acc gag aat gca atc cca gag ttc aag caa aca ctt tcc cgc gcg        1824
Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala
              595                    600                    605
gaa aac atc gac gca atc cac gac gct gtg cag cag atg gct aaa atc        1872
Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile
         610                    615                    620
atc gag agc cag atc aca cac agc ctc ggt cat tca aat tac gac cgt        1920
Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg
625                    630                    635                    640
gtt atc gag ggg ctt ggt act atg cgt gaa gaa ctg gtg gac tat gag        1968
Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu
              645                    650                    655
gaa ccg gcg gtg tac aat gac ttt gtg cgt cag ttg aag ggc aag atg        2016
Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met
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              660                 665                 670
ttg cgg gag gag ctg ggt ggg gat cgg agg gag ctg tgg tgg ttt gta        2064
Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val
        675                 680                 685
agg aag gga aag ctt ggg ctc att ggc aag agt gag gtg gat agc tcg        2112
Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser
        690                 695                 700
gct gtt gag gag caa gag gct caa gag ttt ctg gct ccc aat tga           2157
Ala Val Glu Glu Gln Glu Ala Gln Glu Phe Leu Ala Pro Asn
705                 710                 715
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                20                  25                  30
Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg
        35                  40                  45
Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr
    50                  55                  60
His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu
65                  70                  75                  80
Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln
                85                  90                  95
Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser
                100                 105                 110
Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln
        115                 120                 125
Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile
        130                 135                 140
Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly
145                 150                 155                 160
Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr
                165                 170                 175
Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu
                180                 185                 190
Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr
        195                 200                 205
Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr
    210                 215                 220
Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu
225                 230                 235                 240
Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr
                245                 250                 255
Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly
                260                 265                 270
Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp
        275                 280                 285
Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu
    290                 295                 300
Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys
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305                    310                    315                    320
Gly Tyr Glu Tyr Gly Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu
            325                    330                    335
Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe
        340                    345                    350
Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn
        355                    360                    365
Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser
    370                    375                    380
Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg
385                    390                    395                    400
Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro
            405                    410                    415
Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe
        420                    425                    430
Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile
        435                    440                    445
Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val
    450                    455                    460
Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val
465                    470                    475                    480
Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu
            485                    490                    495
Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg
        500                    505                    510
Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr
    515                    520                    525
Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His
    530                    535                    540
Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys
545                    550                    555                    560
Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly
            565                    570                    575
Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile
        580                    585                    590
Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala
    595                    600                    605
Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile
    610                    615                    620
Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg
625                    630                    635                    640
Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu
            645                    650                    655
Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met
        660                    665                    670
Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val
    675                    680                    685
Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser
    690                    695                    700
Ala Val Glu Glu Gln Glu Ala Gln Glu Phe Leu Ala Pro Asn
705                    710                    715
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